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OM protein - protein search, using sw model

Run on: June 10, 2006, 05:36:37 ; Search time 16 Seconds (without alignments)

Title: US-10-500-428-2

Precise score: 1816

Sequence: 1 MYKDCIESTGDYFLLCDAEQ.....TQECEFIPQAULSPQQDAGGV 345

Scoring table: BL0SUM62 Gapext 0.5

Searched: 64916 seqs, 12643201 residues

Total number of hits satisfying chosen parameters: 64916

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:\*

1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaas/US09\_NEW\_PUB.pep:\*

2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaas/US06\_NEW\_PUB.pep:\*

3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaas/US07\_NEW\_PUB.pep:\*

4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaas/US08\_NEW\_PUB.pep:\*

5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaas/PCT\_NEW\_PUB.pep:\*

6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaas/US10\_NEW\_PUB.pep:\*

7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaas/US11\_NEW\_PUB.pep:\*

8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaas/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	498.5	27.5	403	6 US-10-505-928-203	Sequence 203, App
2	108.5	6.0	1836	7 US-11-313_450-8	Sequence 4512, App
3	102.5	5.6	364	7 US-11-293_697-4612	Sequence 19, App
4	100	5.5	360	7 US-11-242_111-19	Sequence 5124, App
5	97.5	5.4	344	6 US-10-953_349-5324	Sequence 5323, App
6	97.5	5.4	419	6 US-10-953_349-5323	Sequence 5322, App
7	97.5	5.4	513	6 US-10-953_349-5322	Sequence 5321, App
8	97.5	5.4	2005	6 US-10-501_814-3	Sequence 3, App
9	97.5	5.4	2005	7 US-11-263_326-131	Sequence 131, App
10	97.5	5.4	2005	7 US-11-263_326-132	Sequence 132, App
11	97.5	5.4	2005	7 US-11-263_326-175	Sequence 175, App
12	97.5	5.4	2005	7 US-11-263_326-176	Sequence 176, App
13	97.5	5.4	2005	7 US-11-263_326-177	Sequence 177, App
14	97.5	5.4	2005	7 US-11-263_326-178	Sequence 178, App
15	97.5	5.4	2005	7 US-11-263_326-179	Sequence 179, App
16	97.5	5.4	2005	7 US-11-313_450-4	Sequence 4, App
17	96	5.3	2005	7 US-11-263_326-133	Sequence 133, App
18	96	5.3	1980	7 US-11-263_326-128	Sequence 128, App
19	96	5.3	1980	7 US-11-263_326-134	Sequence 134, App
20	96	5.3	1980	7 US-11-313_450-12	Sequence 12, App
21	93.5	5.1	402	6 US-10-471_571A-5294	Sequence 5294, App
22	93.5	5.1	2016	7 US-11-313_450-10	Sequence 10, App
23	92.5	5.1	469	6 US-10-471_571A-5254	Sequence 5254, App
24	92	5.1	2009	7 US-11-263_326-172	Sequence 172, App
25	91.5	5.0	306	6 US-10-953_349-38124	Sequence 38124, A

ALIGNMENTS

Query Match	Best Local Similarity	Score	DB 6;	Length 403;
Qy	12	YFLLCDAEGPGWGLLESAILGIVVTTLLAFLFLMRKIQDCSQNNVLPQLLFLLSVL	7;	Sequence 203, Application US-10-505-928-203
Db	45	YVSLCDLDAIGIVVVAAGAGLITMLLILVRLPFIKEKEKKSPPGLHFLFLGTL	104	General Information: Application No. US20060088532A1
Qy	72	GLFGLAFAFIFELNOQTAPVRYFLFGYLFALCFSCLLAHASHNLVKLYR-GCVSFSTTIL	130	Applicant: Ludwig Institute for Cancer Research et al.
Db	105	GFLGTAFFIOEDETICSVRFLWGVLFALCFSCLLSQANVRRLVRHGTGPAGW-QLV	163	Title of Invention: LYMPHATIC ENDOTHELIAL GENES
Qy	131	CIAIGSLLQIQTATEVTLINTRGMNFVNNTPCQLN-VDFVVLVVVFLMLTTFFVSK	189	File Reference: 28667/3918
Db	164	GLALCLMVQVIAVNLTVLRD----TRPACAYEPMDFTMALLIDMVLLVVTGLAL	219	Current Application Number: US/10/505,928
Qy	190	ATFCGPBENWKHGRFLITVLSIIWWVNISMLLRGNPOFOROPNDPVCIALVNT	249	Prior Application Number: US 60/363, 019
Db	220	FPLCGKFKRWKINGAFLLITAPLSSVLLWAVMTMIFGNVVKLQDGDAWNPDPLA	279	Prior Filing Date: 2004-08-27
Qy	250	AWVFLLIYVPEL-CIYRSRCOECPQGNACPVYQHSFOVNEQELSRSDSGA--	305	Software: PatentIn 3.2
Db	339	GRVFVFLHAIPSIHTCLPALQENTNPFDTSQPRMRETAE-EDQPLRAMEKXFSM	338	SEQ ID NO: 203
				TYPE: PRT
				ORGANISM: Homo sapiens

US-10-505-928-203

GenCore version 5.1.9  
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## OM protein - protein search, using sw model

Run on: June 10, 2006, 05:35:42 ; Search time 178 Seconds

(without alignments)  
897.804 Million cell updates/sec

Title: US-10-500-428-2

Perfect score: 1816

Sequence: 1 MYKDCIESTGDFPLLCDAEQ.....TQEFCFIPQAQKUSPQQDAGGV 345

Scoring table: BLOSUM62

Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters:

2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:  
 1: /EMC\_Celerra\_SIDS3\_ptodata/2/pubbaa/US07\_PUBCOMB.pep.\*  
 2: /EMC\_Celerra\_SIDS3\_ptodata/2/pubbaa/US08\_PUBCOMB.pep.\*  
 3: /EMC\_Celerra\_SIDS3\_ptodata/2/pubbaa/US09\_PUBCOMB.pep.\*  
 4: /EMC\_Celerra\_SIDS3\_ptodata/2/pubbaa/US10A\_PUBCOMB.pep.\*  
 5: /EMC\_Celerra\_SIDS3\_ptodata/2/pubbaa/US10B\_PUBCOMB.pep.\*  
 6: /EMC\_Celerra\_SIDS3\_ptodata/2/pubbaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.

Query

Score

Match

Length

DB ID

Description

Result No.	Score	Match	Length	DB ID	Description
1	1816	100.0	345	4 US-10-225-567A-619	Sequence 619, App
2	1816	100.0	345	4 US-10-600-816-4	Sequence 4, App
3	1816	100.0	345	5 US-10-500-428-2	Sequence 2, App
4	1816	100.0	345	5 US-10-501-841-56	Sequence 56, App
5	1816	100.0	583	5 US-10-505-486-63	Sequence 63, App
6	1816	99.6	345	4 US-10-467-252-8	Sequence 8, App
7	1797.5	99.0	362	4 US-10-182-822A-14	Sequence 14, App
8	1570.5	86.5	323	4 US-10-343-650A-2	Sequence 2, App
9	1570	86.5	300	4 US-10-467-252-9	Sequence 9, App
10	1510	86.5	317	4 US-10-276-774-2644	Sequence 2644, App
11	1318	72.6	300	4 US-10-600-816-5	Sequence 5, App
12	1318	72.6	300	5 US-10-500-428-4	Sequence 4, App
13	1213	66.8	229	4 US-10-029-386-44096.	Sequence 34096, A
14	727.5	40.1	347	3 US-09-866-050A-326	Sequence 326, App
15	727.5	40.1	357	4 US-10-176-847-60	Sequence 60, App
16	727.5	40.1	357	4 US-10-225-567A-454	Sequence 454, App
17	727.5	40.1	357	4 US-10-224-816-4	Sequence 4, App
18	727.5	40.1	357	4 US-10-295-027-620	Sequence 620, App
19	727.5	40.1	357	4 US-10-600-816-3	Sequence 3, App
20	727.5	40.1	357	4 US-10-600-816-17	Sequence 17, App
21	727.5	40.1	357	4 US-10-600-816-20	Sequence 20, App
22	727.5	40.1	357	4 US-10-600-816-21	Sequence 21, App
23	727.5	40.1	357	5 US-10-935-190-21	Sequence 21, App
24	727.5	40.1	357	5 US-10-936-626-118	Sequence 118, App
25	727.5	40.1	357	5 US-10-936-626-142	Sequence 142, App
26	727.5	40.1	357	5 US-10-938-061-18	Sequence 118, App
27	727.5	40.1	357	5 US-10-938-061-142	Sequence 142, App

## ALIGNMENTS

RESULT 1  
 US-10-225-567A-619  
 ; Sequence 619, Application US/10225567A  
 ; Publication No. US20030113798A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lifespan Biosciences  
 ; Brown, Joseph P.  
 ; Burner, Gleanna C.  
 ; Roush, Christine L.  
 ; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR  
 ; FILE REFERENCE: 192-4-4  
 ; CURRENT APPLICATION NUMBER: US/10-225,567A  
 ; PRIORITY FILING DATE: 2001-12-19  
 ; PRIORITY APPLICATION NUMBER: 60/257,144  
 ; NUMBER OF SEQ ID NOS: 2292  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO: 619  
 ; LENGTH: 345  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-225-567A-619

Query Match 100.0%; Score 1816; DB 4;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-154;  
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYKDCIESTGDFPLCDAEQPGNILESLAILGIVVTTILLAFLPLRKIQLDCSQVNVL 60  
 1 MYKDCIESTGDFPLCDAEQPGNILESLAILGIVVTTILLAFLPLRKIQLDCSQVNVL 60  
 61 PTQFLFLISVLGLFGLAFAFELLNQQTAPVRVFLFGVLFALCFSCLLAHASNLVLYRG 120  
 61 PTQFLFLISVLGLFGLAFAFELLNQQTAPVRVFLFGVLFALCFSCLLAHASNLVLYRG 120  
 121 CVFSFWTTILCIAIGCSLQLIITATEYVLTIMTRGMFMVNMTPCQLNVDFWVLLVYVFL 180  
 121 CVFSFWTTILCIAIGCSLQLIITATEYVLTIMTRGMFMVNMTPCQLNVDFWVLLVYVFL 180

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OM protein - protein search, using sw model

Run on: June 10, 2006, 05:34:57 ; Search time 50 Seconds  
 (without alignments)  
 603.961 Million cell updates/sec

Title: US-10-500-428-2  
 Perfect score: 1816

Sequence: 1 MYKDCIESTGDYFLLCDAEG.....TOECAFTPOAKLSPQDDAGGV 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: \* 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters:

650591

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA:\*

1: /EMC\_Celerra\_SIDS3\_ptodata/2/iaa/5\_COMB.pep:  
 2: /EMC\_Celerra\_SIDS3\_ptodata/2/iaa/6\_COMB.pep:  
 3: /EMC\_Celerra\_SIDS3\_ptodata/2/iaa/7\_COMB.pep:  
 4: /EMC\_Celerra\_SIDS3\_ptodata/2/iaa/H\_COMB.pep:  
 5: /EMC\_Celerra\_SIDS3\_ptodata/2/iaa/BCTUS\_COMB.pep:  
 6: /EMC\_Celerra\_SIDS3\_ptodata/2/iaa/RE\_COMB.pep:  
 7: /EMC\_Celerra\_SIDS3\_ptodata/2/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	727.5	40.1	347	2	US-09-188-930-326	Sequence 326, App
2	727.5	40.1	347	2	US-09-312-283C-326	Sequence 326, App
3	727.5	40.1	347	2	US-09-949-016-6443	Sequence 6443, App
4	727.5	40.1	390	2	US-09-949-016-2484	Sequence 9484, App
5	213	11.7	68	2	US-09-118-930-123	Sequence 123, App
6	7	183	10.1	256	2	US-09-312-283C-123
8	164.5	9.1	1027	2	US-09-156-056-85	Sequence 123, App
9.	164.5	9.1	1027	2	US-10-125-051-8	Sequence 8, Appl
10	164.5	9.1	1027	2	US-10-268-051-8	Sequence 8, Appl
11	164.5	9.1	1027	2	US-10-125-778-2	Sequence 2, Appl
12	164.5	9.1	1027	2	US-10-125-792-2	Sequence 2, Appl
13	163	9.0	863	2	US-09-619-353-14	Sequence 14, Appl
14	159.5	8.8	1078	1	US-08-485-588-7	Sequence 7, Appl
20	159.5	8.8	1078	2	US-08-484-159-7	Sequence 7, Appl
21	159.5	8.8	1078	1	US-08-484-565-7	Sequence 7, Appl
22	159.5	8.8	1078	1	US-08-480-751-7	Sequence 7, Appl
17	159.5	8.8	1078	1	US-08-943-986-7	Sequence 7, Appl
18	159.5	8.8	1078	2	US-08-353-784-7	Sequence 7, Appl
19	159.5	8.8	1078	2	US-08-484-719B-7	Sequence 7, Appl
20	159.5	8.8	1078	2	US-10-125-772-28	Sequence 28, Appl
22	159.5	8.8	1078	2	US-10-125-778-28	Sequence 28, Appl
23	159.5	8.8	1078	2	US-10-125-792-28	Sequence 28, Appl
24	159.5	8.8	1088	1	US-08-485-588-6	Sequence 6, Appl
25	159.5	8.8	1088	1	US-08-484-565-6	Sequence 6, Appl
26	159.5	8.8	1088	1	US-08-480-751-6	Sequence 6, Appl

#### ALIGNMENTS

RESULT 1									
US-09-188-930-326									
;	Sequence 326, Application US/09188930A								
;	Patent No. 6150502								
GENERAL INFORMATION:									
;	APPLICANT: Watson, James D.								
;	APPLICANT: Strachan, Lorna								
;	APPLICANT: Sleeman, Matthew								
;	APPLICANT: Onrust, Rene								
;	APPLICANT: Murison, James Greg								
;	TITLE OF INVENTION: Compositions Isolated From Skin Cells								
;	TITLE OF INVENTION: and Methods For Their Use								
;	FILE REFERENCE: 11000.10101C1								
;	CURRENT APPLICATION NUMBER: US/09/188,930A								
;	CURRENT FILING DATE: 1998-11-09								
;	NUMBER OF SEQ ID NOS: 348								
;	SOFTWARE: Fastseq for Windows Version 3.0								
;	SEQ ID NO: 326								
;	LENGTH: 347								
;	TYPE: PRT								
;	ORGANISM: Human								
US-09-188-930-326									

Query Match	40.1%	Score 727.5;	DB 2;	Length 347;
Best Local Similarity	45.7%	Pred. No. 1.4e-62;		
Matches	154;	Conservative 55;	Mismatches 117;	Indels 11;
Gaps	6			
;	1.2 YFLICDAEBSGPWGTTLESIAILGIVTVTILLAAFLFMRKIQDQSQWNVLPQTOLLFLLSVYL			
Qy	YFLICDAEBSGPWGTTLESIAILGIVTVTILLAAFLFMRKIQDQSQWNVLPQTOLLFLLSVYL			
Db	7 YIRLCKDAEAWGIVLVETATAGVTVTSVAFMLTLPILVCKVQDSNRRKPTQFLUQLGVYL			
;	72 GLFCIAFAFILELNOQTAPVRYFLFGVLFAFCPSCLLAHASNUYKLVRGCVSFWSTTLIC			
Qy	GLFCIAFAFILELNOQTAPVRYFLFGVLFAFCPSCLLAHASNUYKLVRGCVSFWSTTLIC			
Db	67 GFLGFLFATTIGLDGSTPTEFLGFLSICFSCLLLAHAVSLTKLVRERKPLSLVLIG			
;	132 IATGCSLQIQLIITAYVTLIMTRG-MMFVNMTPCQLNDVFLVFLMALTFFVSK			
Qy	IATGCSLQIQLIITAYVTLIMTRG-MMFVNMTPCQLNDVFLVFLMALTFFVSK			
Db	727 LAVFSLUQDVIAIEYVILVLTMRNTVNNVFSSELSAPPRNEDFVLLTYFLFLMAITFLMS			
;	190 ATFCGPCECNWKOHGRLLIPITVLSI1IIWVWSMLLRGNPQFOORPQNDPYYVIALVN			
Qy	ATFCGPCECNWKOHGRLLIPITVLSI1IIWVWSMLLRGNPQFOORPQNDPYYVIALVN			
Db	187 FTRCGSF7GPKWKRGAHYLTMU-SIAWVAW-TLMLL-PDFDR-RMDDTILSSALAN			
;	243 GKVFLLAYVSPEFWLTLQRNPMDPYVDAFCPKQPVLYKSYGVENRAYSQEETTQGFET			
Qy	GKVFLLAYVSPEFWLTLQRNPMDPYVDAFCPKQPVLYKSYGVENRAYSQEETTQGFET			
;	250 AWTFLLXYVPECLYRSCLR-QECPLQGNACPVTQHFSQVENQELSRARSDGAE-			
Qy	AWTFLLXYVPECLYRSCLR-QECPLQGNACPVTQHFSQVENQELSRARSDGAE-			

Scoring table:	BLOSUM62	Gapext 10.0 , Gapext 0.5	ALIGNMENTS									
<b>RESULT 1</b>												
GPRC5D_HUMAN STANDARD;												
ID Q9NZD1; Q7Z5J9; Q8TDSS6 ; PRT; 345 AA.												
AC Q9NZD1; Q7Z5J9; Q8TDSS6 ; DT 13-APR-2004, integrated into UniProtKB/Swiss-Prot.												
DT 01-OCT-2000, sequence version 1.												
DT 07-FEB-2006, entry version 26.												
DB G-protein coupled receptor family C group 5 member D.												
GN Name=GPRC5D ;												
OS Homo sapiens (Human).												
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Hominidae;												
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;												
OC Homo .												
OX NCBI_TaxID=9566 ;												
RN RP NUCLEOTIDE SEQUENCE (ISOFORM 1), TISSUE SPECIFICITY, SUBCELLULAR LOCATION, AND INDUCTION.												
RP RC TISSUE-Testis;												
RX MEDLINE-21210966 ; PubMed=11311935 ; Brodin B., Sheppard P.O., Sheppard P.O., Brodin B., Brauner-Osborne H., Jensen A.A., Krogsgaard-Larsen P., O'Hara P.; "Cloning and characterization of a human orphan family C G-protein coupled receptor GPRC5D"; Blochim. Biophys. Acta 1518:237-248 (2001). [1]												
RN RT INOU S., Nanbu T., Shimomura T.; "Characterization of GPRC5D, a member of RAIG family in hard keratinized structures"; Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases. [2]												
RN RT Takeda S., Kadokawa S., Haga T., Takaesu H., Mitaku S.; "Identification of G protein-coupled receptor genes from the human genome sequence"; Genome Lett. 52(0):97-101 (2002). [3]												
RN RT NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA] (ISOFORM 3); MEDLINE-22040966 ; PubMed=12044878; DOI=10.1016/S0014-5793(02)02775-8; Takeda S., Kadokawa S., Haga T., Takaesu H., Mitaku S.; "Identification of G protein-coupled receptor genes from the human genome sequence"; Genome Lett. 52(0):97-101 (2002). [4]												
RN RT NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA] (ISOFORM 1); MEDLINE-22388257 ; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Rahai S.S., Logue N.A., Abramson R.D., Mullay S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Heitman B., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Bouffard G.G., Shevchenko Y., Bouffard G.G.,												
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Minimum DB seq length: 0												
Maximum DB seq length: 2000000000												
Post-processing: Minimum Match 0% Maximum Match 100%												
Database : UniProt 7.2:*												
1: uniprot_sprot:*												
2: uniprot_trembl:*												
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.												
SUMMARIES												
Result No.	Score	Query Match	Length	DB ID	Description							
1	1816	100.0	345	1 GPC5D_HUMAN	Q9nzd1 homo sapien							
2	1816	100.0	345	2 GPC5D_MOUSE	Q3knv3 homo sapien							
3	1494	82.3	344	1 GPC5D_HUMAN	Q3knv3 mus musculus							
4	1494	82.3	344	2 Q3UTY8_MOUSE	Q3uyv8 mus musculus							
5	737	5	40.6	2 Q6PA25_XENLA	Q6pa25 xenopus laevis							
6	727	5	40.1	2 QAI35_HUMAN	Q8nj5s homo sapien							
7	719	5	39.6	2 Q3M806_BOVVIN	Q3mbq6 bos taurus							
8	700	38.5	356	1 QAI33_MOUSE	Q8bb14 mus musculus							
9	549	5	30.3	1 Q5M7X5_XENLR	Q5mk5 xenopus trophophores							
10	540	29.7	468	2 Q2YDG0_BOVVIN	Q2rdg0 bos taurus							
11	531	5	29.3	440	1 GPC5C_MOUSE	Q8kj39 mus musculus						
12	531	5	29.3	457	2 Q3KRC4_RAT	Q3kr4 rattus norvegicus						
13	523	5	28.8	452	2 Q53GM2_HUMAN	Q53gm2 homo sapien						
14	521	5	28.7	441	1 GPC5C_HUMAN	Q9frg8 homo sapien						
15	521	5	28.7	486	2 Q2NLB5_HUMAN	Q2nlb5 homo sapien						
16	504	27.8	432	2 Q5M706_XENTR	Q5m706 xenopus trophophores							
17	498	27.5	403	1 GPC5B_HUMAN	Q9nn51 homo sapien							
18	497	27.4	410	1 GPC5B_MOUSE	Q9n2z0 mus musculus							
19	496	5	27.3	403	2 Q5R9B9_PONY	Q5rb9 pongo pygmaeus						
20	479	5	26.4	403	2 Q5R6C3_PONY	Q5rc3 pongo pygmaeus						
21	443	24.4	393	2 Q4RJM3_TEYING	Q4rjm3 tetrododon nigriventer							
22	424	23.3	353	2 Q4SG16_TEYING	Q4sg16 tetrododon nigriventer							
23	398	5	21.9	349	2 Q4SR12_TEYING	Q4sr12 tetrododon nigriventer						
24	341	18.8	537	2 Q4RZK7_TEYING	Q4rzk7 tetrododon nigriventer							
25	300	5	16.5	188	2 Q5RK14_RAT	Q5rk14 rattus norvegicus						
26	260	5	14.3	262	2 Q9JMP0_MOUSE	Q9jmp0 mus musculus						
27	168	5	9.3	893	1 BOSS_DROSOPHILA	Q2738 drosophila melanogaster						
28	166	5	9.2	1404	2 Q20073_CABEBI	Q20073 caenorhabditis elegans						
29	164	5	9.1	1027	2 Q8J1Q4_SQUID	Q8j1q4 squids acanthocephala						
30	164	9.0	867	1 GPC6A_BRADBURY	Q5ux3 brachydanio							
31	162	5	8.9	896	1 BOSS_DRONE	P22215 drosophila melanogaster						

GenCore version 5.1.9  
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OM protein - protein search, using sw model

\*Run on: June 10, 2006, 05:29:57 ; Search time 41 Seconds  
 (without alignments)  
 809.629 Million cell updates/sec

Title: US-10-500-428-2  
 Perfect score: 1816  
 Sequence: 1 MYKDCIESTGDYFLLCDAEG. ....TQECFIPQAQLSPQQDAGGV 345

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%

Listing first 45 summaries

Database : PIR\_80;\*  
 1: Pir1;\*  
 2: Pir2;\*  
 3: pir3;\*  
 4: pir4;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	168.5		9.3	893	2	A47550 bride of sevenless precursor - hypothetical prote
2	166.5		9.2	1099	2	T16283 hypothetical prote
3	165.5		9.1	896	2	S26740 boss gene
4	162.5		8.9	896	2	A36455 boss protein
5	159.5		8.8	1078	2	A56715 bride of sevenless
6	159.5		8.8	1088	2	B56715 calcium receptor (Ca(2+)-sensing rec)
7	158.5		8.7	1085	2	A40476 calcium/polyvalent metal cation receptor
8	147		8.1	1079	2	T159362 metabotropic Gluta
9	130		7.2	872	2	JH0561 metabotropic Gluta
10	130		7.2	879	2	JC7160 metabotropic Gluta
11	130		7.2	879	2	JH0562 metabotropic Gluta
12	122		6.7	298	2	S15433 hypothetical prote
13	122		6.7	496	2	B22940 hypothetical prote
14	119		6.6	150	2	S43955 probable NADH2 deh
15	116.5		6.4	826	2	T28858 hypothetical prote
16	111		6.1	678	2	B71308 hypothetical prote
17	110		6.1	281	1	S26018 NADH2 dehydrogenas
18	110		6.1	635	1	A64162 cytochrome c-type
19	109.5		6.0	328	1	T112271 NADH2 dehydrogenas
20	109.5		6.0	1840	2	CHRTM1 sodium channel pro
21	109		6.0	288	2	S36954 cytochrome-c oxida
22	109		6.0	288	2	S36955 cytochrome-c oxida
23	108.5		6.0	1835	2	I54323 sodium channel alp
24	108.5		6.0	1836	2	I64853 sodium channel alp
25	105		6.0	1836	2	I51964 sodium channel alp
26	108.5		6.0	1836	2	E22845 hypothetical prote
27	108		5.9	445	2	A46742 metabotropic Gluta
28	108		5.9	871	2	QASGWAVLVLGILPRTLIVR-G cytochrome-c oxida
29	107.5		5.9	287	2	A25877 hypothetical prote

#### ALIGNMENTS

RESULT 1									
A47550									
bride of sevenless precursor - fruit fly (Drosophila virilis)									
N;Alternate names: boss									
C;Species: Drosophila virilis									
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004									
C;Accession: A47550									
R;Hart, A.C.; Harrison, S.D.; Van Vactor Jr., D.L.; Rubin, G.M.; Zipursky, S.L.									
Proc. Natl. Acad. Sci. U.S.A. 90, 5047-5051, 1993									
A;Title: The interaction of bride of sevenless with sevenless is conserved between Dr <sub>c</sub> and Dr <sub>v</sub>									
A;Reference number: A47550; PMID:93281693; PMID:8506350									
A;Status: preliminary									
A;Molecule type: DNA									
A;Gene: FlyBase:vir_boss									
A;Cross-references: UNIPROT:Q24738; UNIPARC:UPI0000126A67; GB:L08132; NID:g290215; PI1									
C;Keywords: transmembrane protein									
Query Match	9.3%	Score	168.5	DB 2;	Length	893;			
Best Local Similarity	21.2%	Pred. No.	3.3e-06;						
Matches	84	Conservative	70;	Mismatches	116;	Indels	127;	Gaps	20;
QY	4	DC1ESTGD--YPLLCDAEGP--WGITLE-----SIAILGIVVTILLLAFLFLMRKI	51						
Db	497	NCQFAGENRRYPLFDESVMWFRKUDTWATGLTAIGLIVTVVRISL	555						
QY	52	QDCSQWNVLPQLFLLSVLGLFLGLAFALFIE-----LNQQTAPVRYF	94						
Db	556	GDYFEGNPV-TSILLISLILYFCSTSYPPFSMEYVGQRNSHVTDFDVTNL-TLGCVRF	613						
QY	95	LFGVLFALCFSCULAHASNLVKL-----VRCGVFSFWTHILC-----IAIGCSLQ	140						
QY	141	III-----ATEYYVLTIMTRGMMFYNMTPCO-----LNYDFVLYLVVFLMLATFF	186						
Db	670	LVVMNHASESVS-----CENIYYGRWLWGLLAYDFLL---CSLVSLYPF	711						
QY	187	VSKATFCGPCTENWKQHGRLLIFTVLSSIIWWYIWMSMLLRGNPQFQROPQWDDPVVCIAL	246						
Db	712	TYRSQ----RNRE-CILIVIGAVLILIIWSWIALSMFGD-----EWRDAAPIGM	758						
QY	247	VNAWVFILLYTVPELCLYRSCQECPQGNACPTAYQHSFQVNEQELSRSDGAE	306						
Db	759	QASGWAVLVLGILPRTLIVR-----IERSDIAOALPS-----	792						
QY	307	EDVALTS--YGTPIQPTVDPTQBCFIPOAKL-SPOQD	341						

Aab68891	Human REC
Aab93311	Human pro
Abr58569	Human can
Abj37054	Human bre
Abj42649	Human GPC
Abp81984	Human GPC
Adg93239	RAIG1_1/
Adn39302	Cancer/an
Adi28460	Human GPC
Ado19632	Human GPC
Adr48222	Human ret
Adr81354	Tumour as
Adt06613	Novel bro
Aea00166	Human TAT
Aea01190	Human TAT
Aea00686	Human TAT
Aea00710	Human TAT
Adc4749	Pancreati
Adx97565	Pancreati
Abp41877	Human ore
Adf70471	Orphan re
Adl28535	Human GPC
24	727.5 40.1 357 4 AAB68891
25	727.5 40.1 357 4 AAB93311
26	727.5 40.1 357 4 ABR58569
27	727.5 40.1 357 6 ABJ37054
28	727.5 40.1 357 6 ABJ42649
29	727.5 40.1 357 6 ABP81984
30	727.5 40.1 357 7 ADG93239
31	727.5 40.1 357 7 ADN39302
32	727.5 40.1 357 8 ADI28460
33	727.5 40.1 357 8 ADO19632
34	727.5 40.1 357 8 ADR48222
35	727.5 40.1 357 8 ADR81354
36	727.5 40.1 357 8 ADD0613
37	727.5 40.1 357 9 AEAO0166
38	727.5 40.1 357 9 AEAO1190
39	727.5 40.1 357 9 AEAO1686
40	727.5 40.1 357 9 AEAO00710
41	727.5 40.1 357 9 AEPA4749
42	727.5 40.1 401 8 ADX97565
43	727.5 40.1 409 5 ABP41877
44	727.5 40.1 595 7 ADFT0471
45	726.5 40.0 357 8 ADL28535
Title:	US-10-500-428-2
Perfect score:	1816
Sequence:	1 MYKDCIESTGDYFLLCDAEG . . . . . TQECCFIPQAKLSPQQDAGGY 345
Scoring table:	BLOSUM62
Gapopen:	10.0 , Gapext 0.5
Searched:	2589679 seqs, 45/216429 residues
Total number of hits satisfying chosen parameters:	2589679
Run on:	June 10, 2006, 05:26:07 ; Search time 199 Seconds (without alignments) 792.662 Million cell updates/sec

**Post-processing:** Minimum Match 100%  
Maximum Match 100%  
Trusting First 45 summaries

Database :	SUMMARIES						Description
	Result No.	Score	Query Match	Length	DB	ID	
A_Geneseq_8:	1:	GeneseqP1980s:	*				Abp81722 Human G-P
	2:	GeneseqP1980s:	*				Abdb0899 Anorexia
	3:	GeneseqP2000s:	*				Abd67579 Human Ly1
	4:	GeneseqP2001s:	*				Add29466 Human GPC
	5:	GeneseqP2002s:	*				Adf70440 Orphan re
	6:	GeneseqP2003as:	*				Aab11329 Human GCR
	7:	GeneseqP2003bs:	*				Adg10857 Human The
	8:	GeneseqP2004s:	*				Aae06764 Human G-P
	9:	GeneseqP2005s:	*				Aab69174 Human G-P
	10:	GeneseqP2006s:	*				Abp95596 Human GPC
							Aab71330 Human GCR
							Adc98222 Human G-P
							Abi12274 Human the
							Adg6101 Skin cell
							Abd80901 Anorexia
							Adc38220 Mouse G-P
							Adc29467 Mouse GPC
							Abd60462 Human Gen
							Aay76071 Rat skin
							Aab56010 Skin cell
							Abb72210 Human pro
							Adi218547 Human GPC
							Adi28461 Human GPC
							Adi22775 Human GPC

RESULT 1

Human G protein-coupled receptor GPRC5D Drotein SEO ID NO:619.  
ABP81722 standard; protein; 345 AA.  
ABP81722;  
04-MAR-2003 (first entry)

ALIGNMENTS

				Aab68891	Human REC
24	727.5	40.1	4	AAB68891	
25	727.5	40.1	4	AAB93311	Human pro
26	727.5	40.1	6	AABP58569	Human can
27	727.5	40.1	6	ABJ37054	Human bre
28	727.5	40.1	6	ABR42649	Human GPC
29	727.5	40.1	6	ABP11984	Human G p
30	727.5	40.1	7	ADD93239	RA1G1. 1/
31	727.5	40.1	7	ADN39302	Cancer /an
32	727.5	40.1	8	ADI128460	Adi28460
33	727.5	40.1	8	ADO29632	Human GPC
34	727.5	40.1	8	ADR48222	Human ret
35	727.5	40.1	8	ADM11254	Tumour as
36	727.5	40.1	8	ADU0613	Novel bro
37	727.5	40.1	9	AEA00166	Human TAT
38	727.5	40.1	9	AEA00190	AEA00190
39	727.5	40.1	9	AEA00686	Human TAT
40	727.5	40.1	9	AEA00710	Human TAT
41	727.5	40.1	9	AED47479	Retroic
42	727.5	40.1	9	ADX97565	Pancreati
43	727.5	40.1	5	ABP41877	Human ova
44	726.5	40.1	5	ADF70471	Orphan re
45	726.5	40.0	5	ADL28535	Human GPC